REMARKS

Favorable reconsideration is respectfully requested in view of the foregoing amendments and the following remarks.

Claims 1 and 6-19 were pending in this application when last examined and stand rejected.

Claims 6-7, 9-10, 12 and 16-19 are cancelled without prejudice or disclaimer thereto.

Claim 20 is newly added. Claims I, 8 and 13 are amended.

Support for phrase "psbA promoter having the nucleotide sequence of SEQ ID NO:7" of amended claim 1 can be found in lines 2-4 of page 19 of the specification. Support for phrase "rps16 terminator having the nucleotide sequence of SEQ ID NO:8" of amended claim 1 can be found in lines 17-18 of page 19 of the specification. Support for phrase "the Rubisco large subunit gene has the nucleotide sequence of SEQ ID NO:15 and the acetyl CoA carboxylase subunit gene has the nucleotide sequence of SEQ ID NO:16" of newly added claim 20 can be found in line 27 on page 22 to line 4 on page 23 of the specification.

Therefore, no new matter has been added.

Re: Claim rejection under USC §103(a)

On pages 2-4 of the Office Action, claims 1 and 6-17 were rejected under 35 U.S.C. 103(a) over Yokota et al. in view of Maliga et al. in view of Palatnik and Gegenbach. Further, on pages 6-9, claims 18 and 19 were rejected under 35 USC 103(a) over Yokota in view of Maliga and McBride. Applicants respectfully traverse these rejections.

(1) Present invention

The gene recombination vector of claim 1 is characterized by the specific combination of limitations of

(1) a DNA fragment comprising a gene encoding a protein having FBPase and SBPase activities which comprises

(a) DNA having the nucleotide sequence of SEQ ID NO: 6;

(b) DNA having a nucleotide sequence in which one nucleotide is deleted, substituted, added or inserted in SEQ ID NO: 6 and encoding a protein having FBPase and SBPase activities; or

(c) DNA hybridizing under stringent conditions with DNA having a nucleotide sequence complementary to the nucleotide sequence of SEQ ID NO: 6 and encoding a protein having FBPase and SBPase activities;

(2) a Rubisco large subunit gene (rbcL);

(3) an acetyl CoA carboxylase subunit gene (accD);

(4) psbA promoter having the nucleotide sequence of SEQ ID NO:7 upstream of the DNA fragment comprising the gene encoding a protein having FBPase and SBPase activities and between the Rubisco large subunit gene and the DNA fragment; and

(5) rps16 terminator having the nucleotide sequence of SEQ ID NO:8 downstream of the DNA fragment comprising the gene encoding a protein having FBPase and SBPase activities and between the DNA fragment and the acetyl CoA carboxylase subunit gene,

wherein the DNA fragment of (1) is between the Rubisco large subunit gene and the acetyl CoA carboxylase subunit gene.

The claimed vector exhibits the following excellent technical effects.

(i) The plant transformed with the claimed vector exhibits enhanced photosynthesis rate (page 10, lines 2-6 of the specification).

(ii) The plant transformed with the claimed vector has excellent height, a large area of leaves and a thick stem. Further, the plant can grow rapidly (page 10, lines 9-14 of the specification).

(2) Rejection of claim 1 over Yokota et al.

Yokota et al. teach a gene recombinant vector having tomato rbcS promoter, S.7942 FBP/SBPase and Nos terminator (paragraph 0017 and Fig.1).

However, Yokota et al. neither teach nor suggest all claimed genes except FBPase/SBPase (claim limitations (2), (3), (4) and (5)).

Further, the rule §1.132 declaration submitted on February 3, 2010 shows that the photosynthesis activity of the transformants with the claimed vector is 1.5 to 1.7-fold higher than that of transformants with the vector of Yokota et al. Thus, the claimed vector has excellent effect unexpectedly superior to the vector of Yokota et al.

Therefore, the inventions of claim 1 and claims 8, 11, 13-15 and 20 depending on claim 1 are unobvious over Yokota et al.

(3) Rejection of claim 1 over Maliga et al.

Maliga et al. disclose the recombinant vector comprising rbcL, psbA(L) promoter, uidA, rps16 terminator and accD (Fig.22C). On the other hand, the claimed vector comprises rbcL, psbA promoter of SEQ ID NO:7, FBPase/SBPase of SEQ ID NO:6, rps16 terminator of SEQ ID NO:8 and accD.

(a) Promoter

Maliga et al. show the nucleotide sequence of psbA(L) promoter in Fig.23A. This nucleotide sequence is different from the nucleotide sequence of psbA promoter of SEQ ID NO:7 of the present invention. The nucleotide sequence alignment attached hereto (Attachment A) shows that psbA(L) promoter of Maliga et al. has surplus regions at both ends and in its sequence which are not found in the psbA promotor of the present invention. The length of the psb(L) promoter of Maliga at al. is 254nt, whereas the length of the psbA promoter of the present invention is 133nt.

(b) Terminator

Maliga et al. show the nucleotide sequence of rps16 terminator in Fig.23K. The nucleotide sequence alignment attached hereto (Attachment B) shows that the nucleotide sequence of the rps16 terminator of Maliga et al. is different from the nucleotide sequence of the rps16 terminator of SEQ ID NO:8 of the present invention in both terminal regions. In addition, the length of the rps16 terminator of Maliga at al. is 166 nt, whereas the length of the rps16 terminator of the present invention is 159 nt.

(c) Target gene

Gene

Target genes of the vectors of the present invention and Maliga et al. are completely different from each other.

Specifically, FBPase/SBPase of the present invention has the nucleotide sequence of SEQ ID NO:6, whereas uidA of Maliga et al. has the nucleotide sequence shown in the web page of GenBank attached hereto (Attachment C). These nucleotide sequences are completely different from each other. The length of FBPase/SBPase of the present invention is 1312nt, whereas the length of uidA is 1809nt (page 1, column "CDS 2551..4359"). Further, as is clear from these

nucleotide sequences, the GC content of FBPase/SBPase of the present invention is 57.4%, whereas the GC content of uidA is 51.4%.

Protein

FBPase/SBPase encoded by FBPase/SBPase of SEQ ID NO:6 of the present invention has an amino acid sequence of SEQ ID NO:5, whereas β-glucronidase encosed by uidA of Maliga et al. has an amino acid sequence shown in the web page of GenBank attached hereto (Attachment D). Both amino acid sequences are completely different from each other. The length of FBPase/SBPase of the present invention is 356aa, whereas the length of β-glucronidase is 602aa. Further, as is clear from these amino acid sequences, the molecular weight of FBPase/SBPase of the present invention is about 40kDa, whereas the molecular weight of β-glucronidase encoded by uidA is about 68kDa.

In addition, functions of the proteins encoded by these genes are completely different.

FBPase/SBPase encoded by FBPase/SBPase of SEQ ID NO:6 is an enzymes functioning in the Calvin cycle of plants. It exhibits fructose 1,6-bisphosphatase activity catalyzing the reaction from fructose 1,6-bisphosphate to fructose 6-bisphosphate and sedoheptulose 1,7-bisphosphatase activity catalyzing the reaction from sedoheptulose 1,7-bisphosphate to sedoheptulose 7-bisphosphate (line 12 on page 1 to line 10 on page 2, lines 24-26 on page 13). On the other hand, β-glucronidase encoded by uidA of Maliga et al. catalyzes the hydrolytic reaction of β-glucronoside (Lines 44-46 on right column of page 3901 of "The EMBO Journal, Vol. 6, No. 13, 3901-3907"; Attachment E). Thus, the both proteins catalyze quite different reactions from each other.

(d) Conclusion

Thus, the promoter, terminator and target gene of the claimed vector are far different from those of Maliga et al. Maliga et al. neither teach nor suggest the specific combination of psbA promoter of SEQ ID NO:7, FBPase/SBPase of SEQ ID NO:6 and rps16 terminator of SEQ ID NO:8 (the specific combination of claim limitations (1), (4) and (5)).

Therefore, it is quite difficult to a person skilled in the art to conceive the claimed invention from Maliga et al.

(4) Rejection of claim 1 over McBride et al.

PsbA promoter of the present invention has the nucleotide sequence of SEQ ID NO:7. On the other hand, McBride et al. are silent about the nucleotide sequence of their psbA promoter (lines 38-40 on column 12). Therefore, McBride et al neither teach nor suggest the claimed psbA promoter (claim limitation (4)).

Further, the rps16 terminator of the present invention has the nucleotide sequence of SEQ ID NO:8. Its length is 159nt. On the other hand, McBride et al. teach that the length of their rps16 terminator is 149nt (lines 5-7 on column 13). Therefore, McBride et al. neither teach nor suggest the claimed rps16 terminator (claim limitation (5)).

In addition, McBride et al. do not teach rcbL, FBPase/SBPase and accD at all (claim limitations (1), (2) and (3)).

Thus, McBride et al. neither teach nor suggest all claim limitations of the present invention. Therefore, it is quite difficult to a person skilled in the art to conceive the claimed invention from McBride et al.

(4) Rejection of claim 1 over Yokota et al. in view of Maliga et al. and McBride et al.

The invention of claim 1 is unobvious over Yokota et al. in view of Maliga et al. and McBride et al. for the following reasons.

(a) Reason 1

As explained above, uidA of Maliga et al. is far different from FBPase/SBPase of Yokota et al. and the invention. Therefore, it would have been unobvious to a person skilled in the art to use FBPase/SBPase of Yokota et al. instead of uidA in the vector of Fig.22C of Maliga et al. to obtain the claimed vector.

(b) Reason 2

As explained above, none of Yokota et al., Maliga et al. and MacBride et al. teach or suggest psbA promoter of SEQ ID NO:7 and rps16 terminator of SEQ ID NO:8 of the present invention (claim limitations (4) and (5)).

Further, expression of a target gene depends on the combination of a promoter and a terminator. For example, this is evidenced by Fig.24B and Fig.25B of Maliga et al. Fig.24B and Fig.25B of Maliga et al. clearly show that uidA expression greatly varies according to the combination of a promoter and a terminator.

In this regard, none of Yokota et al., Maliga et al. and McBride et al. neither teach nor suggest the specific combination of psbA promoter of SEQ ID NO:7 and rps16 terminator of SEQ ID NO:8, above all, the specific combination of psbA promoter of SEQ ID NO:7, FBPase/SBPase of SEQ ID NO:6 and rps16 terminator of SEQ ID NO:8 (specific combination of limitations of (1), (4) and (5)).

Therefore, it is quite difficult to a person skilled in the art to obtain the claimed vector with expectation of high expression of FBPase/SBPase from Yokota et al. in view of Maliga et al. and McBride et al.

Thus, these rejections as applied to the amended claims are untenable and should be withdrawn.

CONCLUSION

In view of the foregoing amendments and remarks, it is respectfully submitted that the present application is in condition for allowance and early notice to that effect is hereby requested.

If the Examiner has any comments or proposals for expediting prosecution, please contact the undersigned attorney at the telephone number below.

Respectfully submitted,

Akiho YOKOTA et al.

/William R. Schmidt, II/
Digitally signed by /William R. Schmidt, II/
DN: cn=/William R. Schmidt, II/, o, ou, email=bschmidt@wenderoth.com, c=US
Date: 2010.12.03 13:16:21 -05'00'

By _____
William R. Schmidt, II
Registration No. 58,327
Attorney for Applicants

WRS/vah
Washington, D.C. 20005-1503
Telephone (202) 721-8200
Facsimile (202) 721-8250
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